Kubelik

#5

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/597,840

DATE: 08/02/2001
TIME: 10:40:35

Input Set : **N:\Crf3\RULE60\09597840.txt**
Output Set: **N:\CRF3\08022001\I597840.raw**

SEQUENCE LISTING

```
  4 (1) GENERAL INFORMATION:
  6      (i) APPLICANT: Qiu, Dewen
  7                    Wei, Zhong-Min
  8                    Beer, Steven V.
 10     (ii) TITLE OF INVENTION: ENHANCEMENT OF GROWTH IN PLANTS
 12    (iii) NUMBER OF SEQUENCES: 10
 14     (iv) CORRESPONDENCE ADDRESS:
 15          (A) ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
 16          (B) STREET: Clinton Square, P.O. Box 1051
 17          (C) CITY: Rochester
 18          (D) STATE: New York
 19          (E) COUNTRY: U.S.A.
 20          (F) ZIP: 14603
 22      (v) COMPUTER READABLE FORM:
 23          (A) MEDIUM TYPE: Floppy disk
 24          (B) COMPUTER: IBM PC compatible
 25          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 28     (vi) CURRENT APPLICATION DATA:
```

C--> 29   **(A) APPLICATION NUMBER: US/09/597,840**
C--> 30   **(B) FILING DATE: 20-Jun-2000**

```
 31          (C) CLASSIFICATION:
 33    (vii) PRIOR APPLICATION DATA:
 34          (A) APPLICATION NUMBER: 09/013,587
 35          (B) FILING DATE:
 37   (viii) ATTORNEY/AGENT INFORMATION:
 38          (A) NAME: Goldman, Michael L.
 39          (B) REGISTRATION NUMBER: 30,727
 40          (C) REFERENCE/DOCKET NUMBER: 19603/1501
 42     (ix) TELECOMMUNICATION INFORMATION:
 43          (A) TELEPHONE: (716) 263-1304
 44          (B) TELEFAX: (716) 263-1600
 47 (2) INFORMATION FOR SEQ ID NO: 1:
 49      (i) SEQUENCE CHARACTERISTICS:
 50          (A) LENGTH: 338 amino acids
 51          (B) TYPE: amino acid
 52          (C) STRANDEDNESS:
 53          (D) TOPOLOGY: linear
 55     (ii) MOLECULE TYPE: protein
 60     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 62     Met Gln Ile Thr Ile Lys Ala His Ile Gly Gly Asp Leu Gly Val Ser
 63     1               5                   10                  15
 65     Gly Leu Gly Ala Gln Gly Leu Lys Gly Leu Asn Ser Ala Ala Ser Ser
 66                     20                  25                  30
 68     Leu Gly Ser Ser Val Asp Lys Leu Ser Ser Thr Ile Asp Lys Leu Thr
 69                     35                  40                  45
```

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/597,840**

DATE: 08/02/2001
TIME: 10:40:35

Input Set : **N:\Crf3\RULE60\09597840.txt**
Output Set: **N:\CRF3\08022001\I597840.raw**

```
71      Ser Ala Leu Thr Ser Met Met Phe Gly Gly Ala Leu Ala Gln Gly Leu
72         50                  55                  60
74      Gly Ala Ser Ser Lys Gly Leu Gly Met Ser Asn Gln Leu Gly Gln Ser
75         65                  70                  75                  80
77      Phe Gly Asn Gly Ala Gln Gly Ala Ser Asn Leu Leu Ser Val Pro Lys
78                          85                  90                  95
80      Ser Gly Gly Asp Ala Leu Ser Lys Met Phe Asp Lys Ala Leu Asp Asp
81                     100                 105                 110
83      Leu Leu Gly His Asp Thr Val Thr Lys Leu Thr Asn Gln Ser Asn Gln
84                 115                 120                 125
86      Leu Ala Asn Ser Met Leu Asn Ala Ser Gln Met Thr Gln Gly Asn Met
87         130                 135                 140
89      Asn Ala Phe Gly Ser Gly Val Asn Asn Ala Leu Ser Ser Ile Leu Gly
90         145                 150                 155                 160
92      Asn Gly Leu Gly Gln Ser Met Ser Gly Phe Ser Gln Pro Ser Leu Gly
93                     165                 170                 175
95      Ala Gly Gly Leu Gln Gly Leu Ser Gly Ala Gly Ala Phe Asn Gln Leu
96                     180                 185                 190
98      Gly Asn Ala Ile Gly Met Gly Val Gly Gln Asn Ala Ala Leu Ser Ala
99                 195                 200                 205
101     Leu Ser Asn Val Ser Thr His Val Asp Gly Asn Asn Arg His Phe Val
102        210                 215                 220
104     Asp Lys Glu Asp Arg Gly Met Ala Lys Glu Ile Gly Gln Phe Met Asp
105     225                 230                 235                 240
107     Gln Tyr Pro Glu Ile Phe Gly Lys Pro Glu Tyr Gln Lys Asp Gly Trp
108                     245                 250                 255
110     Ser Ser Pro Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser Lys
111                     260                 265                 270
113     Pro Asp Asp Asp Gly Met Thr Gly Ala Ser Met Asp Lys Phe Arg Gln
114                 275                 280                 285
116     Ala Met Gly Met Ile Lys Ser Ala Val Ala Gly Asp Thr Gly Asn Thr
117        290                 295                 300
119     Asn Leu Asn Leu Arg Gly Ala Gly Gly Ala Ser Leu Gly Ile Asp Ala
120     305                 310                 315                 320
122     Ala Val Val Gly Asp Lys Ile Ala Asn Met Ser Leu Gly Lys Leu Ala
123                 325                 330                 335
125     Asn Ala
128 (2) INFORMATION FOR SEQ ID NO: 2:
130     (i) SEQUENCE CHARACTERISTICS:
131         (A) LENGTH: 2141 base pairs
132         (B) TYPE: nucleic acid
133         (C) STRANDEDNESS: single
134         (D) TOPOLOGY: linear
136     (ii) MOLECULE TYPE: DNA (genomic)
141     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
143 CGATTTTACC CGGGTGAACG TGCTATGACC GACAGCATCA CGGTATTCGA CACCGTTACG      60
145 GCGTTTATGG CCGCGATGAA CCGGCATCAG GCGGCGCGCT GGTCGCCGCA ATCCGGCGTC     120
147 GATCTGGTAT TTCAGTTTGG GGACACCGGG CGTGAACTCA TGATGCAGAT TCAGCCGGGG     180
149 CAGCAATATC CCGGCATGTT GCGCACGCTG CTCGCTCGTC GTTATCAGCA GGCGGCAGAG     240
```

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/09/597,840**

DATE: 08/02/2001
TIME: 10:40:35

Input Set : **N:\Crf3\RULE60\09597840.txt**
Output Set: **N:\CRF3\08022001\I597840.raw**

```
151 TGCGATGGCT GCCATCTGTG CCTGAACGGC AGCGATGTAT TGATCCTCTG GTGGCCGCTG   300
153 CCGTCGGATC CCGGCAGTTA TCCGCAGGTG ATCGAACGTT TGTTTGAACT GGCGGGAATG   360
155 ACGTTGCCGT CGCTATCCAT AGCACCGACG GCGCGTCCGC AGACAGGGAA CGGACGCGCC   420
157 CGATCATTAA GATAAAGGCG GCTTTTTTTA TTGCAAAACG GTAACGGTGA GGAACCGTTT   480
159 CACCGTCGGC GTCACTCAGT AACAAGTATC CATCATGATG CCTACATCGG GATCGGCGTG   540
161 GGCATCCGTT GCAGATACTT TTGCGAACAC CTGACATGAA TGAGGAAACG AAATTATGCA   600
163 AATTACGATC AAAGCGCACA TCGGCGGTGA TTTGGGCGTC TCCGGTCTGG GGCTGGGTGC   660
165 TCAGGGACTG AAAGGACTGA ATTCCGCGGC TTCATCGCTG GGTTCCAGCG TGGATAAACT   720
167 GAGCAGCACC ATCGATAAGT TGACCTCCGC GCTGACTTCG ATGATGTTTG GCGGCGCGCT   780
169 GGCGCAGGGG CTGGGCGCCA GCTCGAAGGG GCTGGGGGATG AGCAATCAAC TGGGCCAGTC   840
171 TTTCGGCAAT GGCGCGCAGG GTGCGAGCAA CCTGCTATCC GTACCGAAAT CCGGCGGCGA   900
173 TGCGTTGTCA AAAATGTTTG ATAAAGCGCT GGACGATCTG CTGGGTCATG ACACCGTGAC   960
175 CAAGCTGACT AACCAGAGCA ACCAACTGGC TAATTCAATG CTGAACGCCA GCCAGATGAC  1020
177 CCAGGGTAAT ATGAATGCGT TCGGCAGCGG TGTGAACAAC GCACTGTCGT CCATTCTCGG  1080
179 CAACGGTCTC GGCCAGTCGA TGAGTGGCTT CTCTCAGCCT TCTCTGGGGG CAGGCGGCTT  1140
181 GCAGGGCCTG AGCGGCGCGG GTGCATTCAA CCAGTTGGGT AATGCCATCG GCATGGGCGT  1200
183 GGGGCAGAAT GCTGCGCTGA GTGCGTTGAG TAACGTCAGC ACCCACGTAG ACGGTAACAA  1260
185 CCGCCACTTT GTAGATAAAG AAGATCGCGG CATGGCGAAA GAGATCGGCC AGTTTATGGA  1320
187 TCAGTATCCG GAAATATTCG GTAAACCGGA ATACCAGAAA GATGGCTGGA GTTCGCCGAA  1380
189 GACGGACGAC AAATCCTGGG CTAAAGCGCT GAGTAAACCG GATGATGACG GTATGACCGG  1440
191 CGCCAGCATG GACAAATTCC GTCAGGCGAT GGGTATGATC AAAAGCGCGG TGGCGGGTGA  1500
193 TACCGGCAAT ACCAACCTGA ACCTGCGTGG CGCGGGCGGT GCATCGCTGG GTATCGATGC  1560
195 GGCTGTCGTC GGCGATAAAA TAGCCAACAT GTCGCTGGGT AAGCTGGCCA ACGCCTGATA  1620
197 ATCTGTGCTG GCCTGATAAA GCGGAAACGA AAAAAGAGAC GGGGAAGCCT GTCTCTTTTC  1680
199 TTATTATGCG GTTTATGCGG TTACCTGGAC CGGTTAATCA TCGTCATCGA TCTGGTACAA  1740
201 ACGCACATTT TCCCGTTCAT TCGCGTCGTT ACGCGCCACA ATCGCGATGG CATCTTCCTC  1800
203 GTCGCTCAGA TTGCGCGGCT GATGGGGAAC GCCGGGTGGA ATATAGAGAA ACTCGCCGGC  1860
205 CAGATGGAGA CACGTCTGCG ATAAATCTGT GCCGTAACGT GTTTCTATCC GCCCCTTTAG  1920
207 CAGATAGATT GCGGTTTCGT AATCAACATG GTAATGCGGT TCCGCCTGTG CGCCGGCCGG  1980
209 GATCACCACA ATATTCATAG AAAGCTGTCT TGCACCTACC GTATCGCGGG AGATACCGAC  2040
211 AAAATAGGGC AGTTTTTGCG TGGTATCCGT GGGGTGTTCC GGCCTGACAA TCTTGAGTTG  2100
213 GTTCGTCATC ATCTTTCTCC ATCTGGGCGA CCTGATCGGT T                      2141
215 (2) INFORMATION FOR SEQ ID NO: 3:
217      (i) SEQUENCE CHARACTERISTICS:
218           (A) LENGTH: 403 amino acids
219           (B) TYPE: amino acid
220           (C) STRANDEDNESS:
221           (D) TOPOLOGY: linear
223     (ii) MOLECULE TYPE: protein
228     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
230      Met Ser Leu Asn Thr Ser Gly Leu Gly Ala Ser Thr Met Gln Ile Ser
231      1               5                  10                  15
233      Ile Gly Gly Ala Gly Gly Asn Asn Gly Leu Leu Gly Thr Ser Arg Gln
234                  20                  25                  30
236      Asn Ala Gly Leu Gly Gly Asn Ser Ala Leu Gly Leu Gly Gly Asn
237              35                  40                  45
239      Gln Asn Asp Thr Val Asn Gln Leu Ala Gly Leu Leu Thr Gly Met Met
240          50                  55                  60
242      Met Met Met Ser Met Met Gly Gly Gly Gly Leu Met Gly Gly Gly Leu
```

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/597,840

DATE: 08/02/2001
TIME: 10:40:35

Input Set : N:\Crf3\RULE60\09597840.txt
Output Set: N:\CRF3\08022001\I597840.raw

```
243       65                    70                    75                    80
245       Gly Gly Gly Leu Gly Asn Gly Leu Gly Gly Ser Gly Gly Leu Gly Glu
246                        85                    90                    95
248       Gly Leu Ser Asn Ala Leu Asn Asp Met Leu Gly Gly Ser Leu Asn Thr
249                       100                   105                   110
251       Leu Gly Ser Lys Gly Gly Asn Asn Thr Thr Ser Thr Thr Asn Ser Pro
252                       115                   120                   125
254       Leu Asp Gln Ala Leu Gly Ile Asn Ser Thr Ser Gln Asn Asp Asp Ser
255                       130                   135                   140
257       Thr Ser Gly Thr Asp Ser Thr Ser Asp Ser Ser Asp Pro Met Gln Gln
258       145                   150                   155                   160
260       Leu Leu Lys Met Phe Ser Glu Ile Met Gln Ser Leu Phe Gly Asp Gly
261                       165                   170                   175
263       Gln Asp Gly Thr Gln Gly Ser Ser Ser Gly Gly Lys Gln Pro Thr Glu
264                       180                   185                   190
266       Gly Glu Gln Asn Ala Tyr Lys Lys Gly Val Thr Asp Ala Leu Ser Gly
267                       195                   200                   205
269       Leu Met Gly Asn Gly Leu Ser Gln Leu Leu Gly Asn Gly Gly Leu Gly
270       210                   215                   220
272       Gly Gly Gln Gly Gly Asn Ala Gly Thr Gly Leu Asp Gly Ser Ser Leu
273       225                   230                   235                   240
275       Gly Gly Lys Gly Leu Gln Asn Leu Ser Gly Pro Val Asp Tyr Gln Gln
276                       245                   250                   255
278       Leu Gly Asn Ala Val Gly Thr Gly Ile Gly Met Lys Ala Gly Ile Gln
279                       260                   265                   270
281       Ala Leu Asn Asp Ile Gly Thr His Arg His Ser Ser Thr Arg Ser Phe
282                       275                   280                   285
284       Val Asn Lys Gly Asp Arg Ala Met Ala Lys Glu Ile Gly Gln Phe Met
285       290                   295                   300
287       Asp Gln Tyr Pro Glu Val Phe Gly Lys Pro Gln Tyr Gln Lys Gly Pro
288       305                   310                   315                   320
290       Gly Gln Glu Val Lys Thr Asp Asp Lys Ser Trp Ala Lys Ala Leu Ser
291                       325                   330                   335
293       Lys Pro Asp Asp Asp Gly Met Thr Pro Ala Ser Met Glu Gln Phe Asn
294                       340                   345                   350
296       Lys Ala Lys Gly Met Ile Lys Arg Pro Met Ala Gly Asp Thr Gly Asn
297                       355                   360                   365
299       Gly Asn Leu Gln Ala Arg Gly Ala Gly Gly Ser Ser Leu Gly Ile Asp
300       370                   375                   380
302       Ala Met Met Ala Gly Asp Ala Ile Asn Asn Met Ala Leu Gly Lys Leu
303       385                   390                   395                   400
305       Gly Ala Ala
```

308 (2) INFORMATION FOR SEQ ID NO: 4:
310   (i) SEQUENCE CHARACTERISTICS:
311   (A) LENGTH: 1288 base pairs
312   (B) TYPE: nucleic acid
313   (C) STRANDEDNESS: single
314   (D) TOPOLOGY: linear
316   (ii) MOLECULE TYPE: DNA (genomic)

```
321     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
323 AAGCTTCGGC ATGGCACGTT TGACCGTTGG GTCGGCAGGG TACGTTTGAA TTATTCATAA    60
325 GAGGAATACG TTATGAGTCT GAATACAAGT GGGCTGGGAG CGTCAACGAT GCAAATTTCT   120
327 ATCGGCGGTG CGGGCGGAAA TAACGGGTTG CTGGGTACCA GTCGCCAGAA TGCTGGGTTG   180
329 GGTGGCAATT CTGCACTGGG GCTGGGCGGC GGTAATCAAA ATGATACCGT CAATCAGCTG   240
331 GCTGGCTTAC TCACCGGCAT GATGATGATG ATGAGCATGA TGGGCGGTGG TGGGCTGATG   300
333 GGCGGTGGCT TAGGCGGTGG CTTAGGTAAT GGCTTGGGTG GCTCAGGTGG CCTGGGCGAA   360
335 GGACTGTCGA ACGCGCTGAA CGATATGTTA GGCGGTTCGC TGAACACGCT GGGCTCGAAA   420
337 GGCGGCAACA ATACCACTTC AACAACAAAT TCCCCGCTGG ACCAGGCGCT GGGTATTAAC   480
339 TCAACGTCCC AAAACGACGA TTCCACCTCC GGCACAGATT CCACCTCAGA CTCCAGCGAC   540
341 CCGATGCAGC AGCTGCTGAA GATGTTCAGC GAGATAATGC AAAGCCTGTT TGGTGATGGG   600
343 CAAGATGGCA CCCAGGGCAG TTCCTCTGGG GGCAAGCAGC CGACCGAAGG CGAGCAGAAC   660
345 GCCTATAAAA AAGGAGTCAC TGATGCGCTG TCGGGCCTGA TGGGTAATGG TCTGAGCCAG   720
347 CTCCTTGGCA ACGGGGGACT GGGAGGTGGT CAGGGCGGTA ATGCTGGCAC GGGTCTTGAC   780
349 GGTTCGTCGC TGGGCGGCAA AGGGCTGCAA AACCTGAGCG GGCCGGTGGA CTACCAGCAG   840
351 TTAGGTAACG CCGTGGGTAC CGGTATCGGT ATGAAAGCGG GCATTCAGGC GCTGAATGAT   900
353 ATCGGTACGC ACAGGCACAG TTCAACCCGT TCTTTCGTCA ATAAAGGCGA TCGGGCGATG   960
355 GCGAAGGAAA TCGGTCAGTT CATGGACCAG TATCCTGAGG TGTTTGGCAA GCCGCAGTAC  1020
357 CAGAAAGGCC CGGGTCAGGA GGTGAAAACC GATGACAAAT CATGGGCAAA AGCACTGAGC  1080
359 AAGCCAGATG ACGACGGAAT GACACCAGCC AGTATGGAGC AGTTCAACAA AGCCAAGGGC  1140
361 ATGATCAAAA GGCCCATGGC GGGTGATACC GGCAACGGCA ACCTGCAGGC ACGCGGTGCC  1200
363 GGTGGTTCTT CGCTGGGTAT TGATGCCATG ATGGCCGGTG ATGCCATTAA CAATATGGCA  1260
365 CTTGGCAAGC TGGGCGCGGC TTAAGCTT                                     1288
367 (2) INFORMATION FOR SEQ ID NO: 5:
369     (i) SEQUENCE CHARACTERISTICS:
370         (A) LENGTH: 341 amino acids
371         (B) TYPE: amino acid
372         (C) STRANDEDNESS:
373         (D) TOPOLOGY: linear
375     (ii) MOLECULE TYPE: protein
380     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
382     Met Gln Ser Leu Ser Leu Asn Ser Ser Ser Leu Gln Thr Pro Ala Met
383     1               5                   10                  15
385     Ala Leu Val Leu Val Arg Pro Glu Ala Glu Thr Thr Gly Ser Thr Ser
386                     20                  25                  30
388     Ser Lys Ala Leu Gln Glu Val Val Val Lys Leu Ala Glu Glu Leu Met
389                 35                  40                  45
391     Arg Asn Gly Gln Leu Asp Asp Ser Ser Pro Leu Gly Lys Leu Leu Ala
392             50                  55                  60
394     Lys Ser Met Ala Ala Asp Gly Lys Ala Gly Gly Gly Ile Glu Asp Val
395     65                  70                  75                  80
397     Ile Ala Ala Leu Asp Lys Leu Ile His Glu Lys Leu Gly Asp Asn Phe
398                     85                  90                  95
400     Gly Ala Ser Ala Asp Ser Ala Ser Gly Thr Gly Gln Gln Asp Leu Met
401                     100                 105                 110
403     Thr Gln Val Leu Asn Gly Leu Ala Lys Ser Met Leu Asp Asp Leu Leu
404                 115                 120                 125
406     Thr Lys Gln Asp Gly Gly Thr Ser Phe Ser Glu Asp Asp Met Pro Met
407             130                 135                 140
```

VERIFICATION SUMMARY   DATE: 08/02/2001
PATENT APPLICATION: US/09/597,840   TIME: 10:40:36

Input Set : **N:\Crf3\RULE60\09597840.txt**
Output Set: **N:\CRF3\08022001\I597840.raw**

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]